Amendments to the Specification:

Please add the following new paragraph on page 1, before line 5

The present application is a U.S. national phase filing under 35 U.S.C. § 371 of PCT/JP03/03613, filed on March 25, 2003, which claims priority to JP Appl. No. 2002-255442, filed August 30, 2002, the entire disclosures of each of which are hereby incorporated herein by reference for all purposes.

Please replace the paragraph on page 6, lines 5-15 with the following amended paragraph:

The proteins of this invention include proteins comprising an amino acid sequence homology of 50% or more, preferably 70% or more, more preferably 80% or more, even more preferably 90% or more, and most preferably 95% or more (for example, 96%, 97%, 98%, 99%, or more) to the amino acid sequence of SEQ ID NO: 1. Such proteins can be obtained by the above-mentioned site-directed mutagenesis and hybridization method, PCR method (ed. Ausubel et al., Current Protocols in Molecular Biology, publish. John Wiley & Sons, section 6.1-6.4 (1987)), and such. The homologies in this invention are determined using the BLAST algorithm (Karlin and Altschul, Proc. Natl. Acad. Sci. USA 90: 5873-7 (1993)). Programs such as BLASTX (Altschul et al., J. Mol. Biol. 215: 403-10 (1990)) that have been developed based on the BLAST algorithm are known. One can refer to ~~http://~~www.ncbi.nlm.nih.gov**[[.]]** for the specific analytical procedures.

Please replace the paragraph on page 7, lines 21-33 with the following amended paragraph:

The present invention also provides polynucleotides comprising at least 13 consecutive nucleotides complementary to the nucleotide sequence of SEQ ID NO: 2 or its complementary strand. Such complementary polynucleotides do not have to be completely complementary to the nucleotide sequence of SEQ ID NO: 2 or its complementary strand, as long as they have homologies of at least 70% or higher, preferably 80% or higher, more preferably 90% or higher, and even more preferably 95% or higher. Homology can be determined according to the aforementioned methods. Such polynucleotides can be used as probes or primers for the detection and amplification of DNAs and mRNAs encoding the proteins of this invention. When the polynucleotides are used as primers, restriction enzyme recognition sequences and/or tags, for example, can be added to their 5' ends as necessary. The polynucleotides may also be used as antisense ~~nucleotides~~ nucleotide sequences, ribozymes, and such. Antisense ~~nucleotides~~ nucleotide sequences and ribozymes can be used for inhibiting or suppressing the expression of the proteins of this invention.